

RESULT 5

AX127151/c

LOCUS AX127151 349980 bp DNA linear PAT 11-MAY-2001

DEFINITION Sequence 7067 from Patent EP1108790.

ACCESSION AX127151 AX114121

VERSION AX127151.1 GI:14041139

KEYWORDS .

SOURCE Corynebacterium glutamicum

ORGANISM Corynebacterium glutamicum

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE 1

AUTHORS Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.

TITLE Novel polynucleotides

JOURNAL Patent: EP 1108790-A 7067 20-JUN-2001;

KYOWA HAKKO KOGYO CO., LTD. (JP)

FEATURES

Location/Qualifiers

source

1. .349980

/organism="Corynebacterium glutamicum"

/mol_type="genomic DNA"

/db_xref="taxon:1718"

/note="Seq 1 to long (3.309.400) split in 11, seq 7067

2.400.001 2.749.980"

ORIGIN

Query Match 95.4%; Score 2004.4; DB 2; Length 349980;

Best Local Similarity 97.6%; Pred. No. 0;

Matches 2059; Conservative 0; Mismatches 41; Indels 10; Gaps 2;

```

Qy      1  CACAAAATCCGGCGAATCCACCGAAATCGTCTTCATCTTTGGCTTGATCAAATGCCTCAT  60
      |||
Db      228498 CACAAAATCCGGCGAATCCACCGAAATCGTCTTCATCTTTGGCTTGATCAAATGCCTCAT  228439

Qy      61  TCGGCCCGGCTGCACCGTCACGCTTCGAGAAATAGAAATAGCGCTTGTGACGCCACCC-  119
      |||
Db      228438 TCGGCCCGGCTGCACCGTCACGCTTCGAGAAATGAAATAGCGCTTGTGACGCCACCCCT  228379

Qy      120 -----CACTCTCAACGGCAGCCGCCAGCGGTGGCATCAGCCCAGGATTTATTAGGA  171
      |||
Db      228378 CAACGGCAGCCGCCAGCGAGCCTGTGCCAGCGGTGGCATCAGCCCAGGATTTATTAGGA  228319

Qy      172  CCGGCGATATAGGTAATGGAGTGGCACCCTGATCCACCAAATGCACCACAGCCTTCGCC  231
      |||
Db      228318 CCGGCGATATAGGTAATGGAGCGGCACCCCTGATCCACCAAATGCACCACAGCCTTCGGC  228259

Qy      232  GTACCGTCGTAGTTATCCACCATCACGCTGGGAATACCTTGCACTTCACGGCTCATTAA  291
      |||
Db      228258 GCACCGTCGTAGTTATCCACCATCACGCTGGGAATACCTTGCACTTCACGGCTCATTAA  228199

Qy      292  ACAGTGGGAATTTCCCGCGGACTTTGTGGATCTCACCAGAATCCATCCTTGAAGCAGCG  351
      |||
Db      228198 ACAGTGGGAATTTCCCGCGGACTTTGTGGATCTCACCAGAATCCATCCTTGAAGCAGCG  228139

Qy      352  AGCAATAAGCCATCGGCGTGGGGACGATCTTGTCAGCACCTCCCTGGACTTAATCGCC  411
      |||
Db      228138 AGCAATAAGCCATCGGCGTGGGGACGATCTTGTCAGCACCTCCCTGGACTTAATCGCC  228079

Qy      412  GACTCCCGGGCGTCGACAAGCGCAACCGTATAGCCCTGAGTGCTTGCGGCATGCTGCGCG  471
      |||
Db      228078 GACTCCCGGGCGTCGACAAGCGCAACCGTATAGCCCTGAGTGCTTGCGGCATGCTGCGCG  228019

Qy      472  CCCTGGAAAATTTCCAAGAAGAAGGGATTTCGATGCATCGGTGGCAACCATAGCGATGATA  531
      |||
Db      228018 CCCCAGAAAATTTCCAAGAAGAAGGGATTTCGACGCATCGGCGGCAACCATAGCGATGAGG  227959

Qy      532  CCGGTGTTTTGGCGCTGAAAAGCCTGAGTTTCCACACGCGTTGCGGATTTTCTCCGCAGT  591
      |||
Db      227958 CCGGTGTTTTGGCGCTGAAAAGCCTGAGTTTCCACACGCGTTGCGGATTTTCTCCGCAGT  227899

Qy      592  GGAAAACTCACTCGCCAGGCTGCGAAAACGCCCGCGACACAGTGGAAGGGGAGACGCC  651

```

Db	227898	 GGAAAACTCACTCGCCAGGCTGCGAAAACGCCCGGACACAGTGGAAGGGGAGACGCC	227839
Qy	652	AGCGACTTTTGGCAGATCATAAATGGTGGCTTTTGGTGGCTGTG-GCCCCAGAATCTGT	710
Db	227838	AGCGACTTTTGGCAGATCATAAATGGTGGCTTTTGGTGGCTGTGAGCCCCAGAATCTGT	227779
Qy	711	CATGCACAAGAGTATATAGCGCAAAAGAAATCACTAGTCTTGATTCTATGTTGACGATGC	770
Db	227778	CATGCACAAGAGTATATAGCGCAAAAGAAATCACTAGTCTTGATTCTATGTTGACGATGC	227719
Qy	771	CGATACCCGAGTACCTGCACGAAATTTTAGATGATGTCCGCGACACCACCTCCGGCGAGT	830
Db	227718	CGATACCCGAGTACCTGCACGAAATTTTAGATGATGTCCGCGACACCACCTCCGGCGAGT	227659
Qy	831	TGGCCGATTACATCCCGGAACTAAAATCTGCCGACCCAAACCCGCTGGCAGTAGCCCTGT	890
Db	227658	TGGCCGATTACATCCCGGAACTAAAATCTGCCGACCCAAACCCGCTGGCAGTAGCCCTGT	227599
Qy	891	GCACCGTTAACGGACACATCTACAGCGCAGGCGATGACGACATCGAATTCACCATGCAAA	950
Db	227598	GCACCGTTAACGGACACATCTACAGCGCAGGCGATGACGACATCGAATTCACCATGCAAA	227539
Qy	951	GTATTTCCAAGCCCTTTGCTTACGCACTCGCACTCCAAGAATGCGGCTTTGATGAGGTCT	1010
Db	227538	GTATTTCCAAGCCATTTGCTTACGCACTCGCACTCCAAGAATGCGGCTTTGATGAGGTCT	227479
Qy	1011	CTGCATCCGTGGCCTTGGAACCCCTCCGGTGAGGCCTTCAACGAACCTTTCCCTCGACGGCG	1070
Db	227478	CTGCATCCGTGGCCTTGGAACCCCTCCGGTGAGGCCTTCAACGAACCTTTCCCTCGACGGCG	227419
Qy	1071	AAAACCGCCCCATGAACCCCATGATCAACGCCGGCGCGATCGCCATCAACCAGCTGATCA	1130
Db	227418	AAAACCGCCCCATGAACCCCATGATCAACGCCGGCGCGATCGCCATCAACCAGCTGATCA	227359
Qy	1131	ACGGCTCCGACTCCACCGTGGAAGACCGAGTGGAATAATCCGACACTACTTCTCTGAAC	1190
Db	227358	ACGGCTCCGATTCCACCGTGGAAGACCGCGTGGAATAATCCGACACTACTTCTCTGAAC	227299
Qy	1191	TTGCTGGACGCGAACTCACCATCGACCGCGTGCTTGCCGAATCCGAACTCGCCGGCGCGG	1250
Db	227298	TTGCTGGACGCGAACTCACCATCGACCGCGTGCTTGCCGAATCCGAACTCGCCGGCGCGG	227239
Qy	1251	ACCGCAACCTCTCCATCGCCACATGCTGCGCAACTATGGCGTCATCGAAGACGAAGCCC	1310
Db	227238	ACCGCAACCTCTCCATCGCCACATGCTGCGCAATTACGGCGTCATCGAAGACGAAGCCC	227179
Qy	1311	ACGACGCCGTCCTCAGCTACACGCTGCAATGTGCCATCAAAGTAACCACGCGGACCTCG	1370
Db	227178	ACGACGCCGTCCTCAGCTACACGCTGCAATGTGCCATCAAAGTAACCACGCGGACCTCG	227119
Qy	1371	CAGTCATGACCGCCACGCTCGCCGCCGGCGGACGCACCCAATTACCGCAAGAAGCTTC	1430
Db	227118	CAGTCATGACCGCCACGCTCGCCGCCGGCGGACGCACCCAATTACCGCAAGAAGCTTC	227059
Qy	1431	TCGACGCCCGCGTCTGCCGCTCACCCCTCTCCGTCATGGCTTCAGCAGGCATGTACGACG	1490
Db	227058	TCGACGCCCGCGTCTGCCGCTCACCCCTCTCCGTCATGGCTTCAGCAGGCATGTACGACG	226999
Qy	1491	AGGCAGGGCAGTGGCTCTCCACCGTAGGCATCCCCGCGAAATCAGGAGTCGCCGGCGGAC	1550
Db	226998	AGGCAGGGCAGTGGCTCTCCACCGTAGGCATCCCCGCGAAATCAGGAGTCGCCGGCGGAC	226939
Qy	1551	TCATCGGCATTCTGCCAGGTCAGTGGGCATCGCCACATTTTCCCCACGCCTGAACCCCA	1610
Db	226938	TCATCGGCATTCTGCCAGGTCAGTGGGCATCGCCACATTTTCCCCACGCCTGAACCCCA	226879
Qy	1611	AAGGCAACAGCGTGC GCGCGTAAAAATATTCAAACAGCTTTCCGACGACATGGGCCTCC	1670
Db	226878	AAGGCAACAGCGTGC GCGCGTAAAAATATTCAAACAGCTTTCCGACGACATGGGCCTCC	226819

Qy	1671	ACCTTATGTCCACCGAGCAGGTATCCGGCCACGCAGTACGATCCATTACGCGGGACGGCG	1730
Db	226818	ACCTCATGTCCACCGAGCAGGTATCCGGCCACGCAGTACGATCCATCAGCGGGACGGCG	226759
Qy	1731	ACACCACCTTCATCCAAATGCAGGGCGCCATGAACTTCTCAGCCAGCGAAAGCTTCCTCC	1790
Db	226758	ACACCACCTTCATCCAAATGCAGGGCGCCATGAACTTCTCCGCCAGCGAAAGCTTCCTCC	226699
Qy	1791	ACGCCATCGTGGAACACAACCTTTGAAGGCACCGAAGTTGTTCTTGATCTCACCCGAGTAC	1850
Db	226698	ACGCCATCGTGGAACACAACCTTTGAAGGCACCGAAGTTGTTCTTGATCTCACCCGAGTAC	226639
Qy	1851	TTAGCTTCCACCCCGTAGCCATCCGCATGATCAAAGAAGGCCTCAAACGCATCCGCGACG	1910
Db	226638	TTAGCTTCCACCCCGTAGCCATCCGCATGATCAAAGAAGGCCTCAAACGCATCCGCGACG	226579
Qy	1911	CAGGCTTTGAGGTGTTTCATCCTCGACCCAGATGACGTACTGCCCGATTTCATGTTTTCCG	1970
Db	226578	CAGGCTTTGAGGTGTTTCATCCTCGACCCAGATGACGTACTGCCCGATTTCATGTTTTCCG	226519
Qy	1971	ACGGCACCATCTGCAAAGAACGAGTGTGACCGGTAGCTTTATGGTCTGAACAATTCTGAAG	2030
Db	226518	ACGGCACCATCTGCAAAGAACGAGTGTGACCGGTAGCTTTATGGGCTGAACAATTCTAAG	226459
Qy	2031	GAGATTAATCGGTGAAAAAGAAGCTTATGTTGCCTTTGATTGTTGCAGCTTTGGGATTAA	2090
Db	226458	GAGAATTATCCGTGAAAAAGAAGCTTATGTTGCCTTTGATTGTTGCAGCTTTGGGGTTAA	226399
Qy	2091	GTGCCTGCAG	2100
Db	226398	GTGCCTGCAG	226389